AMENDMENTS TO THE CLAIMS

1. - 35. (canceled)

36. (currently amended) A method of identifying a human having an increased risk for developing RF-positive rheumatoid arthritis, comprising determining the identity ~~detecting the presence~~ of a single nucleotide polymorphism (SNP) in said human's nucleic acids as represented by ~~at~~ position 101 of SEQ ID NO: 36673 or its complement ~~thereof in said human's nucleic acids~~, wherein at least one T allele at the SNP based on the sequence orientation of SEQ ID NO:36673 or at least one A allele at the SNP based on the sequence orientation of the complement of SEQ ID NO:36673 ~~the presence of T at position 101 of SEQ ID NO: 36673~~ is indicative of an increased risk for developing said RF-positive rheumatoid arthritis in said human.

37-38. (canceled)

39. (previously presented) The method of claim 36 in which SEQ ID NO: 36673 is contained within the genomic sequence of the PTPN22 gene as represented by SEQ ID NO: 1688.

40. (currently amended) The method of claim 36 in which the SNP ~~to be detected~~ is located at position 42798 of SEQ ID NO: 10739.

41. (previously presented) The method of claim 36 in which said human's nucleic acids are extracted from a biological sample therefrom.

42. (previously presented) The method of claim 41 in which said biological sample is blood.

43. (currently amended) The method of claim 36 in which said human's nucleic acids are amplified before the determining step ~~detection~~ is carried out.

44. (currently amended) The method of claim 36 in which the identity of the SNP is determined ~~detection is carried out~~ by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 49745, SEQ ID NO: 49746, and SEQ ID NO: 49747.

45. (currently amended) The method of claim 36 in which the determining step ~~detection~~ is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

46. (currently amended) A method of identifying a human having a decreased risk for developing RF-positive rheumatoid arthritis, comprising determining the identity ~~detecting the presence~~ of a single nucleotide polymorphism (SNP) in said human's nucleic acids as represented by ~~at~~ position 101 of SEQ ID NO: 36673 or its complement ~~thereof in said human's nucleic acids~~, wherein a homozygous C/C genotype at the SNP based on the sequence orientation of SEQ ID NO:36673 or a homozygous G/G genotype at the SNP based on the sequence orientation of the complement of SEQ ID NO:36673 ~~the presence of C at position 101 of SEQ ID NO: 36673~~ is indicative of a decreased risk for developing said RF-positive rheumatoid arthritis in said human.

47-48. (canceled)

49. (previously presented) The method of claim 46 in which SEQ ID NO: 36673 is contained within the genomic sequence of the PTPN22 gene as represented by SEQ ID NO: 10739.

50. (currently amended) The method of claim 46 in which the SNP ~~to be detected~~ is located at position 42798 of SEQ ID NO: 10739.

51. (previously presented) The method of claim 46 in which said human's nucleic acids are extracted from a biological sample therefrom.

52. (previously presented) The method of claim 51 in which said biological sample is blood.

53. (currently amended) The method of claim 46 in which said human's nucleic acids are amplified before the determining step ~~detection~~ is carried out.

54. (currently amended) The method of claim 46 in which the identity of the SNP is determined ~~detection is carried out~~ by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 49745, SEQ ID NO: 49746, and SEQ ID NO: 49747.

55. (currently amended) The method of claim 46 in which the determining step ~~detection~~ is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

56. (currently amended) A method of determining a human's risk for developing RF-positive rheumatoid arthritis, comprising determining the identity of ~~detecting~~ a single nucleotide polymorphism (SNP) in said human's nucleic acids as represented by ~~at~~ position 101 of SEQ ID NO: 36673 or its complement ~~thereof in said human's nucleic acids~~, wherein at least one T allele at the SNP based on the sequence orientation of SEQ ID NO:36673 or at least one A allele at the SNP based on the sequence orientation of the complement of SEQ ID NO:36673 ~~the presence of T at position 101 of SEQ ID NO: 36673~~ is indicative of an increased risk for developing said RF-positive rheumatoid arthritis in said human, or [[,]] a homozygous C/C genotype at the SNP based on the sequence orientation of SEQ ID NO:36673 or a homozygous G/G genotype at the SNP based on the sequence orientation of the complement of SEQ ID NO:36673 ~~the presence of C at position 101 of SEQ ID NO: 36673~~ is indicative of a decreased risk for developing said RF-positive rheumatoid arthritis in said human.

57-58. (canceled)

59. (previously presented) The method of claim 56 in which SEQ ID NO: 36673 is contained within the genomic sequence of the PTPN22 gene as represented by SEQ ID NO: 10739.

60. (currently amended) The method of claim 56 in which the SNP ~~to be detected~~ is located at position 42798 of SEQ ID NO: 10739.

61. (previously presented) The method of claim 56 in which said human's nucleic acids are extracted from a biological sample therefrom.

62. (previously presented) The method of claim 61 in which said biological sample is blood.

63. (currently amended) The method of claim 56 in which said human's nucleic acids are amplified before the determining step ~~detection~~ is carried out.

64. (currently amended) The method of claim 56 in which the identity of the SNP is determined ~~detection is carried out~~ by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 49745, SEQ ID NO: 49746, and SEQ ID NO: 49747.

65. (currently amended) The method of claim 56 in which the determining step ~~detection~~ is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

66. (new) The method of claim 56, further comprising providing a report of the identity of said SNP.

67. (new) The method of claim 56, further comprising providing a report of said human's risk for developing RF-positive rheumatoid arthritis.

68. (new) The method of claim 67, wherein the risk is an increased risk for developing RF-positive rheumatoid arthritis.

69. (new) The method of claim 67, wherein the risk is a decreased risk for developing RF-positive rheumatoid arthritis.

70. (new) The method of claim 67, wherein the report further shows the identity of said SNP.

71. (new) The method of claim 70, wherein the identity of said SNP is at least one T allele based on the sequence orientation of SEQ ID NO:36673 or at least one A allele based on the sequence orientation of the complement of SEQ ID NO:36673, and wherein the report indicates said human has an increased risk for developing RF-positive rheumatoid arthritis.

72. (new) The method of claim 70, wherein the identity of said SNP is a homozygous C/C genotype based on the sequence orientation of SEQ ID NO:36673 or a homozygous G/G genotype based on the sequence orientation of the complement of SEQ ID NO:36673, and wherein the report indicates said human has a decreased risk for developing RF-positive rheumatoid arthritis.

73. (new) The method of any one of claims 66-72, wherein the report is in paper form or computer readable medium form.